

Sequencing, Finishing, and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM — June 5th - June 7th, 2012

Call for Abstracts (both talks and posters) Deadline March 30th, 2012

Please join us for the 7th annual “Sequencing, Finishing and Analysis in the Future” Meeting on Tuesday, **June 5th through June 7th** in beautiful, historic Santa Fe, New Mexico. The three day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

Keynote Speakers:

- Rita Colwell, Ph.D., Distinguished Professor, University of Maryland & Johns Hopkins University
- Paul Keim, Ph.D., Regents' Professor of Biology, Northern Arizona University
- TBD

Areas to be emphasized include, but are not limited to the following:

Genome Sequencing:

- New sequencing technologies (454, illumina, SOLiD, Ion Torrent, MiSeq, PacBio, etc.)
- Draft sequencing strategies (prokaryotes, eukaryotes, metagenomics, single cell, etc.)
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.

Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies

Genome Finishing:

- Finishing systems and pipelines (automated, manual, etc.)
- Next generation finishing tools and technologies
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Metagenomic analysis



The conference is being sponsored and hosted by the DOE's Los Alamos National Laboratory and **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms are reserved at the La Fonda at a special conference rate of \$83 per night. **A limited number of extra rooms are available before & after the conference for those that want to stay in the area a little longer (contact Chris Detter for more details).**

Registration is limited to 150; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>. Registration will follow the same guidelines as in 2011 (see website for meeting information updates).**

If you have any questions, or would like further information, please contact Chris Detter at (505)667-1326 or cdetter@lanl.gov.

We look forward to seeing you there!!!

The 2012 “Sequencing, Finishing and Analysis in the Future” Organizing Committee:



- * Chris Detter, Ph.D., JGI- LANL, Genomics Center Director, LANL
- * Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- * Patrick Chain, Metagenomics Team Leader, LANL
- * Michael FitzGerald, Finishing Manager, Broad Institute
- * Bob Fulton, M.S., Sequence Improvement Group Leader, WashU
- * Darren Grafham, Team Leader Illumina Bespoke Team, Sanger Institute
- * Alla Lapidus, Ph.D., Director Bioinformatics, IPM, FCCC
- * Donna Muzny, M.S., Director of Operations, BCM
- * Yu-Hui Rogers, VP Core Technology Development, JCVI

